

SEQUENCE LISTINGS

5 SEQ ID NO. 1

SEQ ID No. 1 is the amino acid sequence for HSPDE1B2. For comparative purposes the sequence for HSPDE1B1 is shown in as a comparison using CLUSTAL W (1.74) multiple sequence alignment

10

```
HSPDE1B1  MELSPRSPPEMLEESDCPSFLELKSAPSKMWIKLRSLRLRYMVKQLENGEINIEELKKNL
HSPDE1B2  -----MANPVPVQRSHLQGPILRLR----YMKQLENGEINIEELKKNL
          ..*: :: : : : :*: *****
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15

```
HSPDE1B1  EYTASLLEAVYIDETRQILDTDELQELRSDAVPSEVRDWLASTFTQARAKGRRAEEKP
HSPDE1B2  EYTASLLEAVYIDETRQILDTDELQELRSDAVPSEVRDWLASTFTQARAKGRRAEEKP
          *****
```

20

```
HSPDE1B1  KFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSLNQAADHAL
HSPDE1B2  KFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSLNQAADHAL
          *****
```

25

```
HSPDE1B1  RTIVFELLTRNNLISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTQTVHCFLL
HSPDE1B2  RTIVFELLTRNNLISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTQTVHCFLL
          *****
```

30

```
HSPDE1B1  RTGMVHCLSEIELLAIIFAAAIHDYEHTGTNSFHIQTKSECAIVNDRSVLENHHISSV
HSPDE1B2  RTGMVHCLSEIELLAIIFAAAIHDYEHTGTNSFHIQTKSECAIVNDRSVLENHHISSV
          *****
```

35

```
HSPDE1B1  FRLMQDDENMIFINLTKEFVELRALVIEMVLATDMSCHFQQVKTMKTALQQLERIDKPK
HSPDE1B2  FRLMQDDENMIFINLTKEFVELRALVIEMVLATDMSCHFQQVKTMKTALQQLERIDKPK
          *****
```

40

```
HSPDE1B1  ALSLLLHAADISHPTKQWLVSRTKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
HSPDE1B2  ALSLLLHAADISHPTKQWLVSRTKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
          *****
```

45

```
HSPDE1B1  QIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPSLDVEVGDPNPDVVS
HSPDE1B2  QIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPSLDVEVGDPNPDVVS
          *****
```

```
HSPDE1B1  FRSTWVKRIQENKQKWERAASGITNQMSIDELSPCEEEAPPSPAEDEHNQNGNLD
HSPDE1B2  FRSTWVKRIQENKQKWERAASGITNQMSIDELSPCEEEAPPSPAEDEHNQNGNLD
          *****
```

Sub B13

PCS10350APME

SEQ ID NO. 2

5 SEQ ID No. 2 is the nucleotide sequence for HSPDE1B2. For comparative purposes the sequence for HSPDE1B1 is shown in as a comparison using CLUSTAL W (1.74) multiple sequence alignment

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10 HSPDE1B1      GTCGACCCACGCGTCCGCGCCACGCGTCCGGCCTAGAGACACCGGCCTGGCTGGTCCACGC
HSPDE1B2      GTCGACCCACGCGTCCGGG-AGGAGGAAGGC--AGGGGCCAAAGAGGAAGTTGTCCCTC
          *****  * * *   * * *   * * *   * * *   * * *   * * *

15 HSPDE1B1      CAGCCGCAGACCGTGGCTGAGCATGGAGCTGTCCCCCGCAGTCTCCGGAGATGCTGGA
HSPDE1B2      TTGGGGG---CCCTGGG-GCTCCTGGGG-T--C--AGGATTTGATACTCTGAAGCAGGA
          * *   * * * * *   * * * * *   * *   * * *   * * * * *

20 HSPDE1B1      GGAGTCGGATTGCC--GTCACCCCTGGAGCTGAAGTCAGCCCCAGCAAGAAGATGTGG
HSPDE1B2      A-ACTTTGATTCCCATGGCAAACCTGTTCTGTTCAGAGGAGCCACCTCCAGG-----
          * *   * * * * *   * * * * *   * *   * * *   * * *

25 HSPDE1B1      ATTAAGCTTCGGTCTCTG-CTGCGCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAA
HSPDE1B2      -----GCCCATTTCTCAGGCTGCGCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAA
          * *   * * * * *   * * * * *   * *   * * *   * * *

30 HSPDE1B1      CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTACAT
HSPDE1B2      CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTACAT
          *****

35 HSPDE1B1      AGATGAGACACGGCAAATCTTGGACACGGAGGACGAGCTGCAGGAGCTGCGGTTCAGATGC
HSPDE1B2      AGATGAGACACGGCAAATCTTGGACACGGAGGACGAGCTGCAGGAGCTGCGGTTCAGATGC
          *****

40 HSPDE1B1      CGTGCCCTTCGGAGGTGCGGGACTGGCTGGCCTCCACCTTCACCCAGCAGGCCCGGGCCAA
HSPDE1B2      CGTGCCCTTCGGAGGTGCGGGACTGGCTGGCCTCCACCTTCACCCAGCAGGCCCGGGCCAA
          *****

45 HSPDE1B1      AGGCCGCCGAGCAGAGGAGAAGCCCAAGTCCGAAGCATTGTGCACGCTGTGCAGGCTGG
HSPDE1B2      AGGCCGCCGAGCAGAGGAGAAGCCCAAGTCCGAAGCATTGTGCACGCTGTGCAGGCTGG
          *****

50 HSPDE1B1      GATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTAC
HSPDE1B2      GATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTAC
          *****

55 HSPDE1B1      TGCGGTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGCTTTGATGTCTTTTCTTTGAA
HSPDE1B2      TGCGGTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGCTTTGATGTCTTTTCTTTGAA
          *****

60 HSPDE1B1      CCAGGCAGCAGATGACCATGCCCTGAGGACCATTGTTTTTGTGTTGCTGACTCGGCATAA
HSPDE1B2      CCAGGCAGCAGATGACCATGCCCTGAGGACCATTGTTTTTGTGTTGCTGACTCGGCATAA
          *****

65 HSPDE1B1      CCTCATCAGCCGCTTCAAGATTCCCACCTGTGTTTTGATGAGTTTCTTGGATGCCTTGGA
HSPDE1B2      CCTCATCAGCCGCTTCAAGATTCCCACCTGTGTTTTGATGAGTTTCTTGGATGCCTTGGA
          *****

70 HSPDE1B1      GACAGGCTATGGGAAGTACAAGAATCCTTACCACAACCAGATCCACGCAGCCGATGTTAC
HSPDE1B2      GACAGGCTATGGGAAGTACAAGAATCCTTACCACAACCAGATCCACGCAGCCGATGTTAC
          *****

75 HSPDE1B1      CCAGACAGTCCATTGCTTCTTGCTCCGCACAGGGATGGTGCCTGCTCGGAGATTGA
HSPDE1B2      CCAGACAGTCCATTGCTTCTTGCTCCGCACAGGGATGGTGCCTGCTCGGAGATTGA
          *****

80 HSPDE1B1      GCTCCTGGCCATCATCTTTGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA
HSPDE1B2      GCTCCTGGCCATCATCTTTGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA
          *****

85 HSPDE1B1      CAGCTTCCACATCCAGACCAAGTCAGAATGTGCCATCGTGTACAATGATCGTTCAGTGCT
HSPDE1B2      CAGCTTCCACATCCAGACCAAGTCAGAATGTGCCATCGTGTACAATGATCGTTCAGTGCT
          *****

90 HSPDE1B1      GGAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAGGATGATGAGATGAACATTTT
HSPDE1B2      GGAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAGGATGATGAGATGAACATTTT
          *****

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GenBank accession number: AF010350

PCS10350APME

HSPDE1B1 CATCAACCTCACCAAGGATGAGTTTGTAGAACTCCGAGCCCTGGTCATTGAGATGGTGT
 HSPDE1B2 CATCAACCTCACCAAGGATGAGTTTGTAGAACTCCGAGCCCTGGTCATTGAGATGGTGT

 5
 HSPDE1B1 GGCCACAGACATGTCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA
 HSPDE1B2 GGCCACAGACATGTCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA

 10
 HSPDE1B1 GCTGGAGAGGATTGACAAGCCCAAGGCCCTGTCTCTACTGTCTCATGTGCTGACATCAG
 HSPDE1B2 GCTGGAGAGGATTGACAAGCCCAAGGCCCTGTCTCTACTGTCTCATGTGCTGACATCAG

 15
 HSPDE1B1 CCACCCAACCAAGCAGTGGTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATT
 HSPDE1B2 CCACCCAACCAAGCAGTGGTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATT

 20
 HSPDE1B1 CTTCCTCAGGGTGACAAGGAGGCAGAGTTGGGCCTGCCCTTTTCTCCACTCTGTGACCG
 HSPDE1B2 CTTCCTCAGGGTGACAAGGAGGCAGAGTTGGGCCTGCCCTTTTCTCCACTCTGTGACCG

 25
 HSPDE1B1 CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCAC
 HSPDE1B2 CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCAC

 30
 HSPDE1B1 CAAGTCTAAAAACAGCCAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGG
 HSPDE1B2 CAAGTCTAAAAACAGCCAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGG

 35
 HSPDE1B1 AGACCCCAACCCTGATGTGGTCAGCTTTCGTTCCACCTGGGTCAAGCGCATTGAGGAGAA
 HSPDE1B2 AGACCCCAACCCTGATGTGGTCAGCTTTCGTTCCACCTGGGTCAAGCGCATTGAGGAGAA

 40
 HSPDE1B1 CAAGCAGAAATGGAAGGAACGGGCAGCAAGTGGCATCACCAACCAGATGTCCATTGACGA
 HSPDE1B2 TAAGCAGAAATGGAAGGAACGGGCAGCAAGTGGCATCACCAACCAGATGTCCATTGACGA

 45
 HSPDE1B1 GCTGTCCCCCTGTGAAGAAGAGGCCCCCCCATCCCCGCGGAAGATGAACACAACAGAA
 HSPDE1B2 GCTGTCCCCCTGTGAAGAAGAGGCCCCCCCATCCCCGCGGAAGATGAACACAACAGAA

 50
 HSPDE1B1 TGGGAATCTGGATTAGCCCTGGGGCTGGCCAGGTCTTCATTGAGTCCAAAGTGTGAT
 HSPDE1B2 TGGGAATCTGGATTAGCCCTGGGGCTGGCCAGGTCTTCATTGAGTCCAAAGTGTGAT

 55
 HSPDE1B1 GTCATCAGCACCATCCATCAGGACTGGCTCCCCCATCTGCTCCAAGGAGCGTGGTCGTG
 HSPDE1B2 GTCATCAGCACCATCCATCAGGACTGGCTCCCCCATCTGCTCCAAGGAGCGTGGTCGTG

 60
 HSPDE1B1 GAAGAAACAACCCACCTGAAGGCCAAATGCCAGAGATTGGGGTTGGGGAAGGGCCCTT
 HSPDE1B2 GAAGAAACAACCCACCTGAAGGCCAAATGCCAGAGATTGGGGTTGGGGAAGGGCCCTT

 65
 HSPDE1B1 CCCCACCTGACACCCACTGGGGTGCACTTAAATGTTCCGGCAGCAAGACTGGGGAACCTC
 HSPDE1B2 CCCCACCTGACACCCACTGGGGTGCACTTAAATGTTCCGGCAGCAAGACTGGGGAACCTC

 70
 HSPDE1B1 AGGCTCCAGTGGTCACTGTGCCATCCCTCAGCCTCTGGATTCTCTTCATGGCCAGGTG
 HSPDE1B2 AGGCTCCAGTGGTCACTGTGCCATCCCTCAGCCTCTGGATTCTCTTCATGGCCAGGTG

 75
 HSPDE1B1 GCTGCCAGGGAGCGGGAGCTTCTGAGGCTTCCAGGGCCTTGGGGAAGGGTCAGAGA
 HSPDE1B2 GCTGCCAGGGAGCGGGAGCTTCTGAGGCTTCCAGGGCCTTGGGGAAGGGTCAGAGA

 HSPDE1B1 TGCCAGCCCCCTGGGACCTCCCCCATCCTTTTGCCTCCAAGTTTCTAAGCAATACATTT
 HSPDE1B2 TGCCAGCCCCCTGGGACCTCCCCCATCCTTTTGCCTCCAAGTTTCTAAGCAATACATTT

 HSPDE1B1 TGGGGTTCCCTCAGCCCCCACCCAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTTC
 HSPDE1B2 TGGGGTTCCCTCAGCCCCCACCCAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTTC

PCS10350APME

5 HSPDE1B1 CTCCCTGGGAAGGGCTGGAATAGGATAGAAAGCTGGGGGTTTTCAGAGCCCTATGTGTG
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 10 HSPDE1B1 GGGAGGGGAGTGGATTCTTCAGGGCATGGTACCTTCTAGGACCTGGGAATGGGGTGGG
 HSPDE1B2 GGGAGGGGAGTGGATTCTTCAGGGCATGGTACCTTCTAGGATCTGGGAATGGGGTGGG

 15 HSPDE1B1 TGAATCTTCCTTCCTCCCTTTCTGATATAGTACTGGGGCAAAGGAGCCATTGTGACC
 HSPDE1B2 TGAATCTTCCTTCCTCCCTTTCTGATACAGTACTGGGGCAAAGGAGCCATTGTGACC

 20 HSPDE1B1 AGGGGCTGCGGGAGGCCTTTCCTGGGACCTTCCTTGGGACTGGTCTGGGCCCTGGGGCT
 HSPDE1B2 AGGGGCTGCGGGAGGCCTTTCCTGGGACCTTCCTTGGGACTGGTCTGGGCCCTGGGGCT

 25 HSPDE1B1 TGTGCGCTGCCCTGAGTCCGGAGCCCTTTGCCTCCTTCCTCTCCCCTGGGGCTGGGAGGC
 HSPDE1B2 TGTGCGCTGCCCTGAGTCCGGAGCCCTTTGCCTCCTTCCTCTCCCCTGGGGCTGGGAGGC

 30 HSPDE1B1 TCCATCCGACCAATGTCTGTAAGTGCTTTGAGGATCTCCCCAGCAAAGCACCTTCAGAA
 HSPDE1B2 TCCATCCGACCAATGTCTGTAAGTGCTTTGAGGATCTCCCCAGCAAAGCACCTTCAGAA

 35 HSPDE1B1 TGTATCGACACCAGCTGGGTTAGGGTCAAGGGTGCCTGGGGAGGGTGAGTAATCCTGCAT
 HSPDE1B2 TGTATCGACACCAGCTGGGTTAGGGTCAAGGGTGCCTGGGGAGGGTGAGTAATCCTGCAT

 40 HSPDE1B1 TGCTAAAAGAGAGGGTCTGTCCCCCTCCTCTCCACGTCCCAGAACTGGCCCAGCTGCAGGC
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 45 HSPDE1B1 ACTAAGAAGCTCCTCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG
 HSPDE1B2 ACTAAGAAGCTCCTCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG

 50 HSPDE1B1 GGGCTCAGGGCTGCTGCCTTCCTGTCCTCTGGAGAGAACCAGCCAGGCGCGGTGCCCT
 HSPDE1B2 GGGCTCAGGGCTGCTGCCTTCCTGTCCTCTGGAGAGAACCAGCCAGGCGCGGTGCCCT

 55 HSPDE1B1 TCCTCTCCTCAGGCTCCTCCTTGCCCCACCTTGCCCCAGGAAAGGCCAAAGTCCAGGTG
 HSPDE1B2 TCCTCTCCTCAGGCTCCTCCTTGCCCCACCTTGCCCCAGGAAAGGCCAAAGTCCAGGTG

 60 HSPDE1B1 ACTGCCCTCCTTTCTTTCTGTAATAACCAACCGTGCATTGTACAGTGGGCCCTGTTTCAT
 HSPDE1B2 ACTGCCCTCCTTTCTTTCTGTAATAACCAACCGTGCATTGTACAGTGGGCCCTGTTTCAT

 65 HSPDE1B1 GCGAAATCCACATCCATGGTCTCCTAGACCTGCTACCCTGGTACTTCCACCCTACCCAC
 HSPDE1B2 GCGAAATCCACATCCATGGTCTCCTAGACCTGCTACCCTGGTACTTCCACCCTACCCAC

 HSPDE1B1 CCCGAGAAGGGCAGAGACGCATGTGACTACCCCTGCCCTTGGTTTCCAGACCCCTGCT
 HSPDE1B2 CCCGAGAAGGGCAGAGACGCATGTGACTACCCCTGCCCTTGGTTTCCAGACCCCTGCT

 HSPDE1B1 ACAGCCAGAGAACAATAAAGAAGGGAGACCAGGAAAAAAAAAAAAAAAAAAAAA
 HSPDE1B2 ATAGCCAGAGAACAATAAAGAAGGGAGACCAGGAAAAAAAAAAAAAAAAAAAAA

SEQ ID No. 1

-----MANPVFVQRSHLQGPILRLR-----YVMVKQLENGEINIEELKKNL
EYTSASLEAVYIDETROILDTDEDELQELRSDAVPSEVRDWLASFTTQQRARAKGAAEEK
KFRSIVHVAQAGIFVERMFRRTYTSVGPITYSTAVLNCNLKLDLWCDFDNLQADDDHAL
RTIVFELLTRHNLISRFKIPYTVFLMSFLDALETGYGKYKNPYHNQIHAAVDVTQTVHCFLL
RTGMVHCLSEIELLAIIFAAAIHDYEHTGTTNSFHIQTKSECAIVYNDRSVLNHHISSV
FRLMQDDEMNIFINLTDFEFVELRALVEMVLATDMSCHFQVQKTMKTALQQLERIDKPK
ALSLLHAADDISHPTQOWLVSRRWTKALMEEFFRQGDKEAELGLFFSPLCDRTSTLVAQS
QIGIFIDEVPTFSVLTDVAEKSQVPLADEDSKSNQPSFQWRQPSLDEVGDPNPDVVS
FRSTVWKRIQENKQWKERAASGITNQMSIDELSPCEEAPPSPAEDENQNGNLD

SEQ ID NO. 2

GTGACCCACGCGTCCGGG--AGGAGGAAGGC--AGGGGCCAAAGAGGAAGTTGTCCTCCT
 TTGGGGG---CCCTGGG-GCTCCTGGGG-T-C--AGGATTTTGATACCTGTGAAGCAGGA
 A-ACTTTGTATTCCTACGGCAACCTGTCTCTGTTTCAGAGGAGCCACTCTCAGG-----
 GCCCATTTCTCAGCCTGCCTACATGGTGAAGCATTGGAGAATGGGGAGATAAA
 CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTCTACAT
 AGATGAGACAGCGCAAACTCTGGGACAGGGAGCAGGCTGCGAGAGCTCGGGTGCAGATGC
 CTGCTCTTCGGAGTGTGCGGAGCTGGCTGGCTCCACCTTACCAGCAGGCGCGGGGCCAA
 AGGCGCGCGAGCAGAGGAGAAGCCCAAGTTCGGAAGCATTGTGCACGCTGTGCAGGCTGG
 GATCTTCGTGGAACGGATGTTCCGGAGACATACACCTCTGTGGGCCCCACTTTACTCTAC
 TCGCGTGTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGTCTTGATGTCTTTTCTTGA
 CCAGGCAGAGATGACATTGCTTCCCTGAGGACCATTTGTTTTGAGTTGCTGACTCGGCATAA
 CCTCATCAGCCGCTTCAAGATTCCCACTGTGTTTTTGTAGAGTTTCTTGGATGCTTGGGA
 CAGAGGCTATGGGAAGTACAAGAACTCTTACCAACCAAGCATCCAGCCAGCGGATGTTAC
 CCAGACAGTCCATTGCTTTCTTGTCCGACAGGAGTGTGTCATGCTTGTGCGAGATTGA
 GCTCCTGGCCATCATCTTTGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA
 CAGCTTCCACATCCAGCAAGTCAGAATGTGCCATCGTGTACAATGATCGTTCAGTGTCT
 GGAGAATCACCACCATCAGCTCTGTTTTCCGATGTAGCAGGATGATGAGATGAACATTT
 CATAACCTTACCAGGATGAGTTTTGAGAAGCTCCGAGCCCTGGTCATTGAGATGGTGT
 GGCCACAGACATGTCCTGTCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA
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 CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTTCATGACTTATTGTGGAGCCAC
 AATTCTCTGTGCTGACTGACGTGGCAGAGAAGTGTTCAGCCCTTGGCGGATGAGGACTC
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 GCTGTCCCTCTGTGAAGAAGAGGCCCCCAATCCCCCTCGGAAGATGAACACAACGAA
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 CCCCACCTGACACCCACTGAGGGTGCATTTAATGTTCGGCAGCAAGACTGGGGAACCTC
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 CTGCCAGGGGAGCGGGGAGCTTCTTGAGGCTTCCCAGGGCCTTGGGGAAGGCTCAGAGA
 TGCCAGCCCCCTGGGACCTCCCCATCTTTTGCCTCAAGTTTCTAAGCAATACATTT
 TGGGGGTTCCTCAGCCCCCACCACAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTTC
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 GAGGACATCCTCTTACCCACAGAATTGCGCTGCTTCAGCCCCATCTCCAGCCTGATCCTC
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 GGGCTCAGGGCTGCTGCCTTCTGTCTCTTGGAGAACCCAGCAGCGCGGTGCCCTT
 TCTCTCTCAGGCTCCTCTTCTGCCCTCCTTGCCTCAGGAAGGCCAAAGGCTCAGGCTG
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 GCGAAATCCACATGCTGTGCTCCTAGACCTGCTACCTGGTACTTCCACCTTACCCCTAC
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 ATAGCCGAGAGAACATAAAGAGGGGAGCAGCAAGAAAAAAGAAAAAAGAAAAAAGAAAAA